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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=11; day=4; hr=9; min=21; sec=49; ms=542; ]

=====

\*\*\*\*\*

Reviewer Comments:

<160> 66

Although the above <160> response is "66", 68 sequences are in the submitted file. Please see below:

<210> 68

<211> 10

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 68

Glu Arg Trp Ile Trp Ile Arg Ser Gly Thr

1

5

10

The above is the last sequence in the submitted file.

\*\*\*\*\*

Application No: 10575374 Version No: 2.0

Input Set:

Output Set:

Started: 2009-10-21 17:32:28.305  
Finished: 2009-10-21 17:32:30.540  
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 235 ms  
Total Warnings: 48  
Total Errors: 2  
No. of SeqIDs Defined: 66  
Actual SeqID Count: 68

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)

**Input Set:**

**Output Set:**

**Started:** 2009-10-21 17:32:28.305  
**Finished:** 2009-10-21 17:32:30.540  
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**Actual SeqID Count:** 68

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (38) This error has occurred more than 20 times, will not be displayed
E 252	Calc# of Seq. differs from actual; 66 seqIds defined; count=68

# SEQUENCE LISTING

<110> Ecole Polytechnique Federale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<140> 10575374

<141> 2009-10-21

<150> US 34,404 JM-213

<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 672

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> modified\_base

<222> (186)..(186)

<223> silent point mutation introduced to generate HindIII restriction site

<300>

<308> NCBI / NC\_001136

<309> 2004-08-30

<400> 1

atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgtag 60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180

aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa 240

cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac 300

ggagatgagt cgtggcaaga ataccaagag ttctcgggtt tgccagttat taaaagactc 360

gtattttcaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420

attcccttgt ttgattcaga agcagggtggg acagggtgaac ttttggattg gaactcgatt 480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctgggtgga 540

ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600

agcggagggtg tggagacaaa tgggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa 660

&lt;210&gt; 2

&lt;211&gt; 224

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;300&gt;

&lt;308&gt; NCBI / NC\_001136

&lt;309&gt; 2004-08-30

&lt;400&gt; 2

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln  
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile  
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu  
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile  
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe  
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile  
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met  
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu  
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly  
195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys  
210 215 220

<210> 3  
<211> 132  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> modified\_base  
<222> (22)..(22)  
<223> point mutation

<400> 3  
atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgcag 60  
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
gtgcccaata ga 132

<210> 4  
<211> 44  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg  
35 40

<210> 5  
<211> 540  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 5  
aagagaacaa ttgacccggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa 60  
aatagttcag gcaactccgaa atacttggtt ggcgtgtttc gtaatcaacc taaggaggat 120  
gttttggtc tggatcaatga ttacggcatt gatatcgctc aactgcacgg agatgagtcg 180  
tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa 240  
gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt 300  
gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactggggt 360  
ggaaggcaag agagccccga gagcttacat tttatgtag ctggtggact gacgccagaa 420  
aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggagggtg 480  
gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa 540

<210> 6  
<211> 180  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val  
1 5 10 15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val  
20 25 30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr  
35 40 45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr  
50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys  
65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe  
85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp  
100 105 110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser  
115 120 125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp  
130 135 140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val  
145 150 155 160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys  
165 170 175

Asn Ala Lys Lys  
180

<210> 7  
<211> 159  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 7  
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
gtgcccaata gaaagagaac aattgacccg gttattgca 159

<210> 8  
<211> 53  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
35 40 45

Asp Pro Val Ile Ala  
50

<210> 9  
<211> 516  
<212> DNA



<213> Saccharomyces cerevisiae

<400> 9

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gcaaggaaaa tttcaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac      60
ttggttggcg tgtttcgtaa tcaacctaag gaggatgttt tggctctggt caatgattac      120
ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc      180
ggtttgccag ttattaaaag actcgtatct ccaaaagact gcaacatact actcagtgca      240
gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt      300
gaacttttgg attggaactc gatttctgac tgggttggaa ggcaagagag ccccgagagc      360
ttacatttta tgtagctggg tggactgacg ccagaaaatg ttggtgatgc gcttagatta      420
aatggcggtta ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct      480
aacaaaatag caaatctcgt caaaaatgct aagaaa                                516
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<210> 10

<211> 172

<212> PRT

<213> Saccharomyces cerevisiae

<400> 10

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Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1              5              10              15
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```
Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
              20              25              30
```

```
Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
              35              40              45
```

```
Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
              50              55              60
```

```
Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
65              70              75              80
```

```
Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
              85              90              95
```

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Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
              100             105             110
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Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly  
115 120 125

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile  
130 135 140

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser  
145 150 155 160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys  
165 170

<210> 11  
<211> 561  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 11  
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
gtgcccataa gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180  
aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa 240  
cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac 300  
ggagatgagt cgtggcaaga ataccaagag ttcctcgggt tgccagttat taaaagactc 360  
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420  
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggttg gaactcgatt 480  
tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540  
ctgacgccag aaaatgttgg t 561

<210> 12  
<211> 187  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln  
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile  
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu  
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile  
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe  
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile  
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met  
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly  
180 185

<210> 13  
<211> 111  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 13  
gatgcgctta gattaaatgg cgttattggt gttgatgtaa gcggaggtgt ggagacaaat 60  
ggtgtaaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a 111

<210> 14  
<211> 37  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly  
1 5 10 15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val  
20 25 30

Lys Asn Ala Lys Lys  
35

<210> 15

<211> 612

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (22)..(22)

<223> point mutation

<220>

<221> deletion

<222> (612)..(612)

<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAG  
ACTCT

<400> 15

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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120  
gtgcccataa gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180  
aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa 240  
cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300  
ggagatgagt cgtggcaaga ataccaagag ttcctcgggt tgccagttat taaaagactc 360  
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420  
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttgattg gaactcgatt 480  
tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga 540  
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600  
agcggaggtg tg 612

<210> 16

<211> 204  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 16

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val  
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp  
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile  
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys  
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln  
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile  
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu  
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile  
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe  
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile  
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met  
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu  
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val  
195 200

<210> 17  
 <211> 36  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*  
  
 <220>  
 <221> mutation  
 <222> (1)..(1)  
 <223> missing sequence before base 1 of SEQ17, corresponding to base 63  
 7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17  
 aacaaaaatag caaatcttcgt caaaaatgct aagaaa 36

<210> 18  
 <211> 12  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys  
 1 5 10

<210> 19  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> first of a pair of peptides (together with peptide C2), that asso-  
 ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),  
 12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala  
 1 5 10 15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu  
 20 25 30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly  
 35 40

<210> 20  
 <211> 50  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> second of a pair of peptides (together with peptide C1), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu  
1 5 10 15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys  
20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp